

O I P E

777

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/670,756A

DATE: 07/05/2001
TIME: 10:39:36

Input Set : A:\seqlistcorrected.txt
Output Set: N:\CRF3\07052001\I670756A.raw

3 <110> APPLICANT: Rhodes, Kenneth
4 Betty, Maria
5 Ling, Huai-Ping
6 An, Wengqian
8 <120> TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
10 <130> FILE REFERENCE: MNI-070CP4
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/670,756A
13 <141> CURRENT FILING DATE: 2000-09-27
15 <150> PRIOR APPLICATION NUMBER: USSN 60/110,277
16 <151> PRIOR FILING DATE: 1998-11-30
18 <150> PRIOR APPLICATION NUMBER: USSN 60/110,033
19 <151> PRIOR FILING DATE: 1998-11-25
21 <150> PRIOR APPLICATION NUMBER: USSN 60/109,333
22 <151> PRIOR FILING DATE: 1998-11-20
24 <150> PRIOR APPLICATION NUMBER: USSN 09/298,731
25 <151> PRIOR FILING DATE: 1999-04-23
27 <150> PRIOR APPLICATION NUMBER: USSN 09/350,614
28 <151> PRIOR FILING DATE: 1999-07-09
30 <150> PRIOR APPLICATION NUMBER: USSN 09/350,874
31 <151> PRIOR FILING DATE: 1999-07-09
33 <150> PRIOR APPLICATION NUMBER: USSN 09/400,492
34 <151> PRIOR FILING DATE: 1999-09-21
36 <150> PRIOR APPLICATION NUMBER: USSN 09/399,913
37 <151> PRIOR FILING DATE: 1999-09-21
39 <150> PRIOR APPLICATION NUMBER: PCT/US99/27428
40 <151> PRIOR FILING DATE: 1999-11-19
43 <160> NUMBER OF SEQ ID NOS: 73
45 <170> SOFTWARE: PatentIn Ver. 2.0
47 <210> SEQ ID NO: 1
48 <211> LENGTH: 1463
49 <212> TYPE: DNA
50 <213> ORGANISM: Homo sapiens
52 <220> FEATURE:
53 <221> NAME/KEY: CDS
54 <222> LOCATION: (225)..(872)
56 <400> SEQUENCE: 1
58 qaatacgccc ctttcaacttc ttagtccctg catgtgcggg gctqaagaag qaagccagaa 60
+
See page

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74	25	30	35	
76	gag gga ctg gag cag ctc gag gcc cag acc aac ttc acc aag agg gag			380
77	Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu			
78	40	45	50	
80	ctg cag gtc ctt tat cga ggc ttc aaa aat gag tgc ccc agt ggt gtg			428
81	Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val			
82	55	60	65	
84	gtc aac gaa gac aca ttc aag cag atc tat gct cag ttt ttc cct cat			476
85	Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His			
86	70	75	80	
88	gga gat gcc agc acg tat gcc cat tac ctc ttc aat gcc ttc gac acc			524
89	Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr			
90	85	90	95	100
92	act cag aca ggc tcc gtg aag ttc gag gac ttt gta acc gct ctg tcg			572
93	Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser			
94	105	110	115	
96	att tta ttg aga gga act gtc cac gag aaa cta agg tgg aca ttt aat			620
97	Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn			
98	120	125	130	
100	ttg tat gac atc aac aag gac gga tac ata aac aaa gag qaq atq atq			668
101	Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met			
102	135	140	145	
104	gac att gtc aaa gcc atc tat gac atg atg ggg aaa tac aca tat cct			716
105	Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro			
106	150	155	160	
108	gtg ctc aaa gag gac act cca agg cag cat gtg gac gtc ttc ttc cag			764
109	Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln			
110	165	170	175	180
112	aaa atg gac aaa aat aaa gat ggc atc gta act tta gat gaa ttt ctt			812
113	Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu			
114	185	190	195	
116	gaa tca tgt cag gag gac aac atc atq agg tct ctc cag ctg ttt			860
117	Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe			
118	200	205	210	
120	caa aat qtc atg taactqqtqa cactcaqcca ttcaqctctc agagacattg			912
121	Gln Asn Val Met			
122	215			
124	tactaaacaa ccaccttaac accctgatct gcccttggc tgattttaca caccactct			972
126	tgggacagaaa acacccctta cactttggaa gaattctctg ctgaagactt tctttatggaa			1032
128	cccaagcatca tggggctcag tctctgattt ccaactcttc ctctttcttc ttcttgagag			1092
130	agacaagatg aaatttgagt ttgttttggaa agcatgctca tctccctcaca ctgctgccct			1152
132	atqqaaggta cctctqctta aqcttaaaca qtaqtqacaa aaatatqctq cttaqctqcc			1212
145	<210> SEQ ID NO: 2			
146	<211> LENGTH: 216			

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147 <212> TYPE: PRT
 148 <213> ORGANISM: Homo sapiens
 150 <400> SEQUENCE: 2

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 152 1 5 10 15
 154 Arg Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val
 155 20 25 30
 157 Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
 158 35 40 45
 160 Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 161 50 55 60
 163 Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
 164 65 70 75 80
 166 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 167 85 90 95
 169 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 170 100 105 110
 172 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
 173 115 120 125
 175 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 176 130 135 140
 178 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 179 145 150 155 160
 181 Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
 182 165 170 175
 184 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
 185 180 185 190
 187 Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
 188 195 200 205
 190 Leu Gln Leu Phe Gln Asn Val Met
 191 210 215
 194 <210> SEQ ID NO: 3
 195 <211> LENGTH: 1856
 196 <212> TYPE: DNA
 197 <213> ORGANISM: Rattus sp.
 199 <220> FEATURE:
 200 <221> NAME/KEY: CDS
 201 <222> LOCATION: (300)..(1034)
 203 <400> SEQUENCE: 3
 204 qgcacacaac ccttggattc ttccggaaat atgccgttag gtgttgccaa ttatataatc 60
 206 tttggctag cagatgttta gggactgggt aagccttgg agaaattacc ttagaaaaac 120
 208 qaaqaaataa aaqcaaaatg taccatgaaat tqcaaqatta cctaaqcaatt qcaaaqtaaq 180
 215 Met Pro Ala Asp Val Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
 216 1 5 10 15
 218 caq qgc gac tct gaa ggg ctc cag acc ttg ggg ata gta qtg qtc ctg 395
 219 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Leu

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220	20	25	30	
222	tgt tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att qac ttg tcg			443
223	Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser			
224	35	40	45	
226	gat gac aag atc gag gat gat ctg gag atg acc atg gtt tgc cat cgg			491
227	Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg			
228	50	55	60	
230	cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc aag aga			539
231	Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg			
232	65	70	75	80
234	gaa ctg caa gtc ctt tac cgg gga ttc aaa aac gag tgc ccc agt ggt			587
235	Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly			
236	85	90	95	
238	gtg gtt aac gaa gag aca ttc aag cag atc tac gct cag ttt ttc cct			635
239	Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro			
240	100	105	110	
242	cat gga gat gcc agc aca tac gca cat tac ctc ttc aat gcc ttc gac			683
243	His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp			
244	115	120	125	
246	acc acc cag aca ggc tct qta aag ttc gag gac ttt gtq act gct ctg			731
247	Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu			
248	130	135	140	
250	tcg att tta ctg aga gga acg gtc cat gaa aaa ctg agg tgg acg ttt			779
251	Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe			
252	145	150	155	160
254	aat ttg tac gac atc aat aaa gac ggc tac ata aac aaa gag gag atg			827
255	Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met			
256	165	170	175	
258	atg gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat			875
259	Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr			
260	180	185	190	
262	cct gtg ctc aaa gag gac act ccc agg caq cac gtg qac gtc ttc ttc			923
263	Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe			
264	195	200	205	
266	caq aaa atq qat aaa aat aaa qat qqc att qta acg tta gac qaa ttt			971
267	Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe			
268	210	215	220	
270	ctc gag tcc tgt cag gag gat gac aac atc atg agg tct cta cag ctg			1019
271	Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu			
272	225	230	235	240
274	ttc caa aat gtc atg taactgagga cactggccat cctgctctca gagacactga			1074
275	Phe Gln Asn Val Met			

282	caqgtqgtc aqgtgtgtgt tggcaactct tcttcctcc tcttcttqat aqaaacaaqgc	1254
284	tgaaatccqa aqttttgtttt qgaaqcatgc ccatctctcc atgtgtgtgc tgcctgtqq	1314
286	aaggccccctc tqcttgagct taaacagtag tgcacagttt tctgcgtata cagatccccca	1374
288	actcaactqcc tctaaqtcaq qcaqaccctg atcaatctga accaaatqtq caccatcctc	1434

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240 ccatggcctc ccaagccaat gtgcgtgtt ctcttcctct ggtggaaaga aqaaacgctc 1494
 242 tacaqagcac ttagagctta ccatgaaaat actgggagag gcagcaccta acacatgtag 1554
 244 aataggactg aattatataag catgggttgc tcagatgtat caaacagccc atgtcatttt 1614
 246 ttttccaga ggttagggact aataattctc ccacactagc acctacgatc atagaacaag 1674
 248 tcttttaaca catccaggag gaaaaccgtt gcccagtgtt ctatcccttc tctccatccc 1734
 300 ctqctcaagc ccagcaactgc atgtctctcc cgaaaggctc agaatgcctg taaaaatgctg 1794
 302 taacttttat accctgttat aatcaataaa cagaactatt tcgtacaaaa aaaaaaaaaa 1854
 304 aa 1856

307 <210> SEQ ID NO: 4
 308 <211> LENGTH: 245
 309 <212> TYPE: PRT
 310 <213> ORGANISM: Rattus sp.
 312 <400> SEQUENCE: 4

313 Met Pro Ala Arg Val Leu Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
 314 1 5 10 15
 316 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
 317 20 25 30
 319 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
 320 35 40 45
 322 Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
 323 50 55 60
 325 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
 326 65 70 75 80
 328 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
 329 85 90 95
 331 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
 332 100 105 110
 334 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
 335 115 120 125
 337 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
 338 130 135 140
 340 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
 341 145 150 155 160
 343 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
 344 165 170 175
 346 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
 347 180 185 190
 349 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
 350 195 200 205
 352 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
 353 210 215 220
 354 Asn Ile Asn Asp Asp Asn Ile Met Arg Ser Leu Gln Leu

362 <210> SEQ ID NO: 5

363 <211> LENGTH: 1907

364 <212> TYPE: DNA

365 <213> ORGANISM: Mus musculus

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:3017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:3356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43